Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: 09/355,254 |
|---|---|---|

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

| | | |
|---|---|---|
| 1 | Wrapped Nucleics<br>Wrapped Aminos | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping." |
| 2 | Invalid Line Length | The rules require that a line not exceed 72 characters in length. This includes white spaces. |
| 3 | Misaligned Amino Numbering | The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead. |
| 4 | Non-ASCII | The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text. |
| 5 | Variable Length | Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing. |
| 6 | PatentIn 2.0 "bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences. |
| 7 | Skipped Sequences (OLD RULES) | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:<br>(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)<br>(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)<br>(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)<br>This sequence is intentionally skipped<br><br>Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. |
| 8 | Skipped Sequences (NEW RULES) | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.<br><210> sequence id number<br><400> sequence id number<br>000 |
| 9 | Use of n's or Xaa's (NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing.<br>Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.<br>In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. |
| 10 ✓ | Invalid <213> Response | Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence |
| 11 | Use of <220> | Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.<br>Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.<br>(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules) |
| 12 | PatentIn 2.0 "bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk. |
| 13 | Misuse of n | n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide. |

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RAW SEQUENCE LISTING DATE: 07/03/2002
PATENT APPLICATION: US/09/355,254E TIME: 12:17:28

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Input Set : N:\Crf3\Refhold\I355254.raw
Output Set: N:\CRF3\07032002\I355254E.raw

<110> APPLICANT: Wagner, Hermann
Lipford, Grayson
Heeg, Klaus
<120> TITLE OF INVENTION: Pharmaceutical Compositions Comprising a Polynucleotide and Optionally an Antigen Especially for Vaccination
<130> FILE REFERENCE: C1041/7005 (AWS)
<140> CURRENT APPLICATION NUMBER: US/09/355,254E
<141> CURRENT FILING DATE: 2002-04-30
<150> PRIOR APPLICATION NUMBER: PCT/EP98/00367
<151> PRIOR FILING DATE: 1998-01-23
<150> PRIOR APPLICATION NUMBER: EP 97101019.4
<151> PRIOR FILING DATE: 1997-01-23
<160> NUMBER OF SEQ ID NOS: 27
<170> SOFTWARE: FastSEQ for Windows Version 3.0

Does Not Comply
Corrected Diskette Needed

(global Error)

<210> SEQ ID NO: 1
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Genomic DNA

See item 10 on Error Summary sheet

<400> SEQUENCE: 1
tcattggaaa acgttcttcg gggc 24

<210> SEQ ID NO: 2
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Genomic DNA
<400> SEQUENCE: 2
accgatgacg tcgccggtga cggcaccacg 30

<210> SEQ ID NO: 3
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligopeptide
<400> SEQUENCE: 3
Ser Ile Ile Asn Phe Glu Lys Leu
1 5

<210> SEQ ID NO: 4
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Genomic DNA
<400> SEQUENCE: 4
tccatgacgt tcctgatgct 20

<210> SEQ ID NO: 5

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<211> LENGTH: 20
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attgcctgac gtcagagagc 20

<210> SEQ ID NO: 6
<211> LENGTH: 20
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<213> ORGANISM: Genomic DNA
<400> SEQUENCE: 6
tccatgacgt cactgatgct 20

<210> SEQ ID NO: 7
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<400> SEQUENCE: 7
attgcctgac gttcgagagc 20

<210> SEQ ID NO: 8
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<400> SEQUENCE: 8
gattgcctga cgtcagagag 20

<210> SEQ ID NO: 9
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<212> TYPE: DNA
<213> ORGANISM: Genomic DNA
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<210> SEQ ID NO: 10
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<400> SEQUENCE: 10
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<212> TYPE: DNA
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<400> SEQUENCE: 11
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<210> SEQ ID NO: 12
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<213> ORGANISM: Genomic DNA
<400> SEQUENCE: 12
tcgatcgggg cggggcgagc 20

<210> SEQ ID NO: 13
<211> LENGTH: 20

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Input Set : N:\Crf3\Refhold\I355254.raw
Output Set: N:\CRF3\07032002\I355254E.raw

106 <212> TYPE: DNA
107 <213> ORGANISM: Genomic DNA
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111 <210> SEQ ID NO: 14
112 <211> LENGTH: 20
113 <212> TYPE: DNA
114 <213> ORGANISM: Genomic DNA
115 <400> SEQUENCE: 14
116 agcgggggcg agcgggggcg 20
118 <210> SEQ ID NO: 15
119 <211> LENGTH: 24
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121 <213> ORGANISM: Genomic DNA
122 <400> SEQUENCE: 15
123 tactttcagt ttcatattac tcta 24
125 <210> SEQ ID NO: 16
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127 <212> TYPE: DNA
128 <213> ORGANISM: Genomic DNA
129 <400> SEQUENCE: 16
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132 <210> SEQ ID NO: 17
133 <211> LENGTH: 20
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135 <213> ORGANISM: Genomic DNA
136 <400> SEQUENCE: 17
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139 <210> SEQ ID NO: 18
140 <211> LENGTH: 20
141 <212> TYPE: DNA
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147 <211> LENGTH: 20
148 <212> TYPE: DNA
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150 <400> SEQUENCE: 19
151 ctgatttccc cgaaatgatg 20
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157 <400> SEQUENCE: 20
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160 <210> SEQ ID NO: 21
161 <211> LENGTH: 20
162 <212> TYPE: DNA

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Input Set : N:\Crf3\Refhold\I355254.raw
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<213> ORGANISM: Genomic DNA
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<210> SEQ ID NO: 22
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<212> TYPE: DNA
<213> ORGANISM: Genomic DNA
<400> SEQUENCE: 22
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<210> SEQ ID NO: 23
<211> LENGTH: 20
<212> TYPE: DNA
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<400> SEQUENCE: 23
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<210> SEQ ID NO: 24
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Genomic DNA
<400> SEQUENCE: 24
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<210> SEQ ID NO: 25
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Genomic DNA
<400> SEQUENCE: 25
caaaaaaatt tccagtcctt 20

<210> SEQ ID NO: 26
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<212> TYPE: DNA
<213> ORGANISM: Genomic DNA
<400> SEQUENCE: 26
atgttttcct gcgttgccag 20

<210> SEQ ID NO: 27
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Genomic DNA
<400> SEQUENCE: 27
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/03/2002
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Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 22
Seq#:2; Line(s) 29
Seq#:4; Line(s) 46
Seq#:5; Line(s) 53
Seq#:6; Line(s) 60
Seq#:7; Line(s) 67
Seq#:8; Line(s) 74
Seq#:9; Line(s) 81
Seq#:10; Line(s) 88
Seq#:11; Line(s) 95
Seq#:12; Line(s) 102
Seq#:13; Line(s) 109
Seq#:14; Line(s) 116
Seq#:15; Line(s) 123
Seq#:16; Line(s) 130
Seq#:17; Line(s) 137
Seq#:18; Line(s) 144
Seq#:19; Line(s) 151
Seq#:20; Line(s) 158
Seq#:21; Line(s) 165
Seq#:22; Line(s) 172
Seq#:23; Line(s) 179
Seq#:24; Line(s) 186
Seq#:25; Line(s) 193
Seq#:26; Line(s) 200
Seq#:27; Line(s) 207

VERIFICATION SUMMARY DATE: 07/03/2002
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